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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/955,572CDATE: 02/28/2000
TIME: 15:36:25

Input Set: H955572C.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

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1 <110> APPLICANT: Kwon, Byoung
2 <120> TITLE OF INVENTION: NEW RECEPTOR AND RELATED PRODUCTS AND
3 METHODS
4 <130> FILE REFERENCE: 740.013US2
5 <140> CURRENT APPLICATION NUMBER: US/08/955,572C
6 <141> CURRENT FILING DATE: 1997-10-22
7 <150> EARLIER APPLICATION NUMBER: 08/461,652
8 <151> EARLIER FILING DATE: 1995-06-05
9 <150> EARLIER APPLICATION NUMBER: 08/122,796
10 <151> EARLIER FILING DATE: 1993-09-03
11 <160> NUMBER OF SEQ ID NOS: 12
12 <170> SOFTWARE: FastSEQ for Windows Version 3.0
13 <210> SEQ ID NO 1
14 <211> LENGTH: 838
15 <212> TYPE: DNA
16 <213> ORGANISM: Homo sapiens
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19 catagtagcc actctgttgc tggcctcaa ctttgagagg acaagatcat tgcaggatcc 120
20 ttgtagtaac tgcccagctg gtacattctg tgataataac aggaatcaga tttgcagtcc 180
21 ctgtcctcca aatagtttct ccagcgcagg tggacaaagg acctgtgaca tatgcaggca 240
22 gtgtaaagggt gttttcagga ccaggaagga gtgttcctcc accagcaatg cagagtgtga 300
23 ctgcactcca gggtttcact gcctgggggc aggatgcagc atgtgtgaac aggattgtaa 360
24 acaagggtcaa gaactgacaa aaaaagggtg taaagactgt tgctttggga catttaacga 420
25 tcagaaacgt ggcactctgc gacctggac aaactgttct ttggatggaa agtctgtgct 480
26 tgtgaatggg acgaaggaga gggacgtggt ctgtggacca tctccagctg acctctctcc 540
27 gggagcatcc tctgtgaccc cgctgcccc tgcgagagag ccaggacact ctccgcagat 600
28 catctccttc tttcttgccg tgacgtcgac tgcgttgctc ttctgtctgt tcttctcac 660
29 gctccgtttc tctgttggtt aacggggcag aaagaaactc ctgtatatat tcaaacaacc 720
30 atttatgaga ccagtacaaa ctactcaaga ggaagatggc tgtagctgcc gatttccaga 780
31 agaagaagaa ggaggatgtg aactgtgaaa tggaagtcaa tagggctgtt gggacttt 838
32 <210> SEQ ID NO 2
33 <211> LENGTH: 255
34 <212> TYPE: PRT
35 <213> ORGANISM: Homo sapiens
36 <400> SEQUENCE: 2
37 Met Gly Asn Ser Cys Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu
38 1 5 10 15
39 Asn Phe Glu Arg Thr Arg Ser Leu Gln Asp Pro Cys Ser Asn Cys Pro
40 20 25 30
41 Ala Gly Thr Phe Cys Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys
42 35 40 45
43 Pro Pro Asn Ser Phe Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile
44 50 55 60
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45      Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser
46      65                                70                                75                                80
47      Thr Ser Asn Ala Glu Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly
48                                85                                90                                95
49      Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu
50                                100                               105                               110
51      Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln
52                                115                               120                               125
53      Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys
54                                130                               135                               140
55      Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro
56      145                                150                                155                                160
57      Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Val Thr Pro Pro Ala
58                                165                                170                                175
59      Pro Ala Arg Glu Pro Gly His Ser Pro Gln Ile Ile Ser Phe Phe Leu
60                                180                                185                                190
61      Ala Leu Thr Ser Thr Ala Leu Leu Phe Leu Leu Phe Phe Leu Thr Leu
62                                195                                200                                205
63      Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
64                                210                                215                                220
65      Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
66      225                                230                                235                                240
67      Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
68                                245                                250                                255

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69      <210> SEQ ID NO 3
70      <211> LENGTH: 20
71      <212> TYPE: DNA
72      <213> ORGANISM: Homo sapiens
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74      ttytgymgaa artayaaycc
75      <210> SEQ ID NO 4
76      <211> LENGTH: 20
77      <212> TYPE: DNA
78      <213> ORGANISM: Homo sapiens
79      <400> SEQUENCE: 4
80      ttytcstsca htggtggaca
81      <210> SEQ ID NO 5
82      <211> LENGTH: 20
83      <212> TYPE: DNA
84      <213> ORGANISM: Homo sapiens
85      <400> SEQUENCE: 5
86      cccargswrc aggttytrca
87      <210> SEQ ID NO 6
88      <211> LENGTH: 20
89      <212> TYPE: DNA
90      <213> ORGANISM: Homo sapiens
91      <400> SEQUENCE: 6
92      ttytgrtcrt traatgttcc
93      <210> SEQ ID NO 7
94      <211> LENGTH: 25

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95 <212> TYPE: DNA
96 <213> ORGANISM: Homo sapiens
97 <400> SEQUENCE: 7
98     aataagcttt gctagtatca tacct                                25
99 <210> SEQ ID NO 8
100 <211> LENGTH: 30
101 <212> TYPE: DNA
102 <213> ORGANISM: Homo sapiens
103 <400> SEQUENCE: 8
104     ttaagatctc tgcggagagt gtcctggctc                                30
105 <210> SEQ ID NO 9
106 <211> LENGTH: 2350
107 <212> TYPE: DNA
108 <213> ORGANISM: Mus musculus
109 <220> FEATURE:
110 <221> NAME/KEY: unsure
111 <222> LOCATION: (1253)...(1255)
112 <223> OTHER INFORMATION: (a or g or c or t/u)
113 <400> SEQUENCE: 9
114     atgtccatga actgctgagt ggataaacag cacgggatat ctctgtctaa aggaatatta    60
115     ctacaccagg aaaaggacac attcgacaac aggaaaggag cctgtcacag aaaaccacag    120
116     tgtcctgtgc atgtgacatt tcgccatggg aaacaactgt tacaacgtgg tggtcattgt    180
117     gctgctgcta gtgggctgtg agaaggtggg agccgtgcag aactcctgtg ataactgtca    240
118     gcctggtact ttctgcagaa aatacaatcc agtctgcaag agctgccctc caagtacctt    300
119     ctccagcata ggtggacagc cgaactgtaa catctgcaga gtgtgtgcag gctatttcag    360
120     gttcaagaag ttttgtcctt ctaccacaaa cgcggagtggt gagtgcattg aaggattcca    420
121     ttgcttgggg ccacagtgcg ccagatgtga aaaggactgc aggcctggcc aggagctaac    480
122     gaagcagggg tgcaaaacct gtagcttggg aacattttaat gaccagaacg gtactggcgt    540
123     ctgtcgaccc tggacgaact gctctctaga cgggaaggtct gtgcttaaga cggggaccac    600
124     ggagaaggac gtggtgtgtg gacccctgtg ggtgagcttc tctcccagta ccaccatttc    660
125     tgtgactcca gagggaggac caggagggca ctccctgcag gtccttacct tgttcctggc    720
126     gctgacatcg gctttgctgc tggccctgat cttcattact ctccgtttct ctgtgtcaa    780
127     atggatcagg aaaaaattcc cccacatatt caagcaacca tttaagaaga cactggagc    840
128     agctcaagag gaagatgctt gtagctgccg atgtccacag gaagaagaag gaggaggagg    900
129     aggctatgag ctgtgatgta ctatcctagg agatgtgtgg gccgaaaccg agaagcacta    960
130     ggacccacc atcctgtgga acagcacaag caacccacc accctgttct tacacatcat    1020
131     cctagatgat gtgtgggcgc gcacctcatc caagtctctt ctaacgctaa catatttgct    1080
132     tttacctttt ttaaattctt ttttaattt aaattttatg tgtgtgagtg ttttgctgct    1140
133     ctgtatgcac acgtgtgtgt gtgtgtgtgt gtgacactcc tgatgcctga ggaggtcaga    1200
134     agacaaaggg ttggttccat aagaactgga gttatggatg gctgtgagcc ggnngatag    1260
135     gtcgggacgg agacctgtct tcttatttta acgtgactgt ataataaaaa aaaaatgata    1320
136     tttcgggaat tgtagagatt gtccctgacac ccttctagtt aatgatctaa gaggaattgt    1380
137     tgatacgtag tatactgtat atgtgtatgt atatgtatat gtatatataa gactctttta    1440
138     ctgtcaaagt caacctagag tgtctggtta ccaggtcaat tttattggac attttacgtc    1500
139     acacacacac acacacacac acacacacgt ttatactacg tactgttatc ggtattctac    1560
140     gtcataataat gggatagggg aaaaggaaac caaagagtga gtgatattat tgtggagggtg    1620
141     acagactacc ccttctgggt acgtagggac agacctcctt cggactgtct aaaactcccc    1680
142     ttagaagtct cgtcaagttc ccggacgaag aggacagagg agacacagtc cgaagagtta    1740
143     tttttccggc aaatcctttc cctgtttcgt gacactccac cccttgtgga cacttgagtg    1800
144     tcctccttgc gccggaaggt caggtggtac ccgtctgtag gggcggggag acagagccgc    1860

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W-->OK

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145      ggggggagcta cgagaatcga ctcacagggc gccccgggct tcgcaaatga aactttttta      1920
146      atctcacaag tttcgtccgg gctcggcgga cctatggcgt cgatccttat taccttatcc      1980
147      tggcgccaag ataaaaacaac caaaagcctt gactccggta ctaattctcc ctgccggccc      2040
148      ccgtaagcat aacgcggcga tctccacttt aagaacctgg ccgcgttctg cctgggtctcg      2100
149      ctttcgtaaa cggttcttac aaaagtaatt agttcttgct ttcagcctcc aagcttctgc      2160
150      tagtctatgg cagcatcaag gctggtatatt gctacggctg accgctacgc cgccgcaata      2220
151      aggggtactgg gcggcccgtc gaaggccctt tggtttcaga aacccaaggc cccctcata      2280
152      ccaacgtttc gactttgatt cttgccggta cgtgggtggtg ggtgccttag ctctttctcg      2340
153      atagttagac                                     2350
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155      <211> LENGTH: 256
156      <212> TYPE: PRT
157      <213> ORGANISM: Mus musculus
158      <400> SEQUENCE: 10
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160      1          5          10          15
161      Gly Cys Glu Lys Val Gly Ala Val Gln Asn Ser Cys Asp Asn Cys Gln
162      20          25          30
163      Pro Gly Thr Phe Cys Arg Lys Tyr Asn Pro Val Cys Lys Ser Cys Pro
164      35          40          45
165      Pro Ser Thr Phe Ser Ser Ile Gly Gly Gln Pro Asn Cys Asn Ile Cys
166      50          55          60
167      Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys Phe Cys Ser Ser Thr
168      65          70          75          80
169      His Asn Ala Glu Cys Glu Cys Ile Glu Gly Phe His Cys Leu Gly Pro
170      85          90          95
171      Gln Cys Thr Arg Cys Glu Lys Asp Cys Arg Pro Gly Gln Glu Leu Thr
172      100         105         110
173      Lys Gln Gly Cys Lys Thr Cys Ser Leu Gly Thr Phe Asn Asp Gln Asn
174      115         120         125
175      Gly Thr Gly Val Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Arg
176      130         135         140
177      Ser Val Leu Lys Thr Gly Thr Thr Glu Lys Asp Val Val Cys Gly Pro
178      145         150         155         160
179      Pro Val Val Ser Phe Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu
180      165         170         175
181      Gly Gly Pro Gly Gly His Ser Leu Gln Val Leu Thr Leu Phe Leu Ala
182      180         185         190
183      Leu Thr Ser Ala Leu Leu Leu Ala Leu Ile Phe Ile Thr Leu Leu Phe
184      195         200         205
185      Ser Val Leu Lys Trp Ile Arg Lys Lys Phe Pro His Ile Phe Lys Gln
186      210         215         220
187      Pro Phe Lys Lys Thr Thr Gly Ala Ala Gln Glu Glu Asp Ala Cys Ser
188      225         230         235         240
189      Cys Arg Cys Pro Gln Glu Glu Glu Gly Gly Gly Gly Tyr Glu Leu
190      245         250         255
191      <210> SEQ ID NO 11
192      <211> LENGTH: 24
193      <212> TYPE: PRT
194      <213> ORGANISM: Homo sapiens

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195 <220> FEATURE:
196 <221> NAME/KEY: ZN_FING
197 <222> LOCATION: 2...3, 5...13, 15...17, 19...21, 23
198 <223> OTHER INFORMATION: Putative zinc finger structure
199 <400> SEQUENCE: 11
W- 200 Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa
W- 201 1 5 10 15
202 Xaa His Xaa Xaa Xaa Cys Xaa Cys
203 20
204 <210> SEQ ID NO 12
205 <211> LENGTH: 12
206 <212> TYPE: PRT
207 <213> ORGANISM: Homo sapiens
208 <400> SEQUENCE: 12
209 Leu Gln Asp Pro Cys Ser Asn Cys Pro Ala Gly Thr
210 1 5 10

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VERIFICATION SUMMARY
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DATE: 02/28/2000
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Line	? Error/Warning	Original Text
134	W "N" or "Xaa" used: Feature required	agacaaaggg ttggttccat aagaactgga gttatgga
200	W "N" or "Xaa" used: Feature required	Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa X
202	W "N" or "Xaa" used: Feature required	Xaa His Xaa Xaa Xaa Cys Xaa Cys